

Substitute Form PTO-1449
(Modified)U.S. Department of Commerce
Patent and Trademark OfficeAttorney's Docket No.
16380-002001Application No.
09/877,695**Information Disclosure Statement
by Applicant**

(Use several sheets if necessary)

Applicant
John R. DesjarlaisFiling Date
June 8, 2001Group Art Unit
1631**U.S. Patent Documents**

Examiner Initial	Desig. ID	Document Number	Publication Date	Patentee	Class	Subclass	Filing Date If Appropriate
<i>MS</i>	AA	US 6,188,965	Feb. 13, 2001	Mayo et al.			
<i>MS</i>	AB	US 6,269,312	Jul. 31, 2001	Mayo et al.			
<i>MS</i>	AC	US 6,403,312	Jun. 11, 2002	Dahiyat et al.			
<i>MS</i>	AD	US 2002/0123846	Sep. 5, 2002	Miller et al.			
	AE						
	AF						
	AG						
	AH						
	AI						
	AJ						
	AK						

Foreign Patent Documents or Published Foreign Patent Applications

Examiner Initial	Desig. ID	Document Number	Publication Date	Country or Patent Office	Class	Subclass	Translation	
							Yes	No
	AL							
	AM							
	AN							
	AO							
	AP							

Other Documents (include Author, Title, Date, and Place of Publication)

Examiner Initial	Desig. ID	Document
	AQ	
	AR	
	AS	
	AT	

Examiner Signature

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Date Considered

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	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	Translation	
						YES	NO

OTHER DOCUMENTS (including Author, Title, Date, Pertinent Pages, Etc.)

msm	Shaojian Sun. "Reduced representation model of protein structure prediction: Statistical potential and genetic algorithms." <i>Protein Science</i> . (1993), 2, 762-785.
msm	Fujiyoshi-Yoneda. "Adaptability of restrained molecular dynamics for tertiary structure prediction: application to Crotalus atrox venom phospholipase A2." <i>Protein Engineering</i> . (1991), Vol. 4, 443-450.
msm	International Search Report. PCT/US02/03789, mailed January 22, 2003.

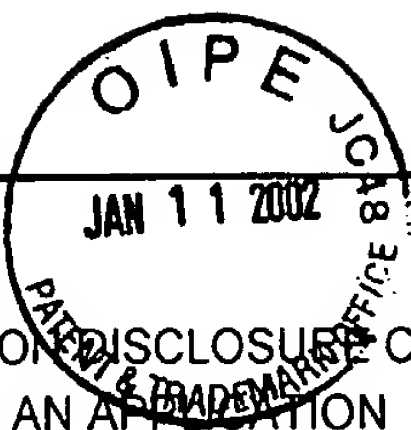
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msy	Dahiyat et al. "Automated design of the surface positions of protein helices." <i>Protein Science</i> . (1997), 6: 1333-1337.
msy	Dahiyat et al. "Protein design automation." <i>Protein Science</i> . (1996), 5: 895-903.
msy	Dahiyat et al. "De novo protein design: Fully automated sequence selection." <i>Science</i> . Vol. 278, 3 Oct. 1997, 82-87.

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ms	Dahiyat et al. "Probing the role of packing specificity in protein design." <i>Proc. Natl. Acad. Sci. USA</i> . Vol. 94, 10172-10177, Sept. 1997.
ms	Dahiyat et al. "De novo protein design: Towards fully automated sequence selection." <i>J. Mol. Biol.</i> (1997) 273, 789-796.
ms	Delarue et al. "The inverse protein folding problem: Self consistent mean field optimisation of a structure specific mutation matrix." <i>Pac Symp Biocomput.</i> (1997), 109-121.

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OTHER DOCUMENTS (including Author, Title, Date, Pertinent Pages, Etc.)

msj	Desjarlais et al. "Computer Search Algorithms in protein modification and design." (1998) <i>Curr Opin Struct Biol.</i> 8(4), 471-5.
msj	Desjarlais et al. "De novo design of the hydrophobic cores of proteins." <i>Protein Science</i> (1995), 4, 2006-18.
msj	Desjarlais et al. "Side-chain and backbone flexibility in protein core design. <i>J. Mol. Biol.</i> (1999), 290(1), 305-18.

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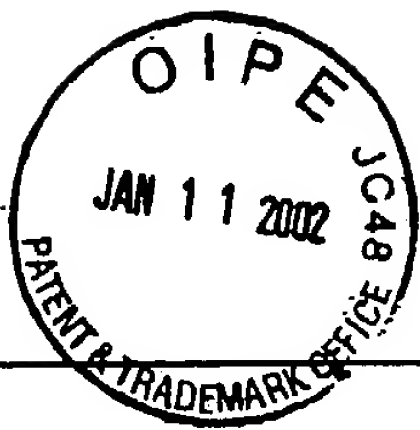
	DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	Translation	
						YES	NO

OTHER DOCUMENTS (including Author, Title, Date, Pertinent Pages, Etc.)

msy	Desmet et al., "The dead-end elimination theorem and its use in protein side-chain positioning." <i>Nature</i> . (1992), 356(9), 539-542.
msy	Dunbrack et al. "Bayesian statistical analysis of protein side-chain rotamer preferences. <i>Protein Sci.</i> (1997), 6(8), 1661-81.
msy	Eisenberg et al., "Solvation energy in protein folding and binding." <i>Nature</i> . 319(6050), 199-203. 1986

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msm	Goldstein. "Efficient rotamer elimination applied to protein side-chains and related spin glasses. <i>Biophys. J.</i> (1994), 66(5), 1335-40.
msm	Gordon. "Energy functions for protein design. <i>Curr Opin Struct Biol.</i> (1999), 9(4), 509-13.
msm	Harbury et al. "Repacking protein cores with backbone freedom: structure prediction for coiled coils." <i>Proc Natl Acad Sci USA.</i> (1995), 92(18), 8408-12.

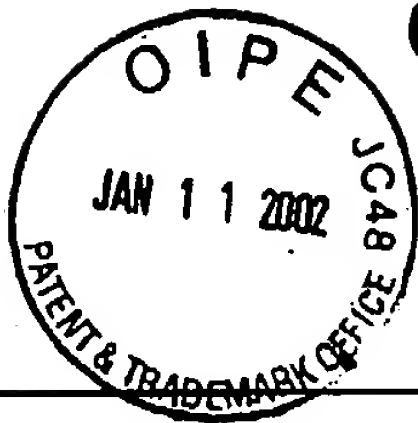
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msy	Hellinga. "Rational protein design: combining theory and experiment." <i>Proc Natl Acad Sci USA</i> . (1997), 94(19), 10015-17.
msy	Hellinga et al. "Optimal sequence selection in proteins of known structure by simulated evolution." <i>Proc Natl Acad Sci USA</i> . (1994), 91(13), 5803-7.
msy	Hendsch et al. "Electrostatic interactions in the GCN4 leucine zipper: Substantial contributions arise from intramolecular interactions enhanced on binding. <i>Protein. Sci.</i> (1999), 8(7), 1381-92.

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msm	Henikoff et al. "Position-based sequence weights. <i>J. Mol. Biol.</i> (1994), 243(4), 574-8.
msm	Holland. <i>Adaptation in natural and artificial systems</i> . The MIT Press, Cambridge, MA (1992).
msm	Johnson et al. "Solution structure and dynamics of a designed hydrophobic core variant of ubiquitin. <i>Structure Fold Des.</i> (1999), 7(8), 967-76.

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	Jorgensen et al. "The OPLS potential functions for proteins. Energy minimizations for crystals of cyclic peptides and crambin." <i>J. Amer. Chem. Soc.</i> (1988), 110(6), 1657-1666.
	Koehl et al. "Application of a self-consistent mean field theory to predict protein side-chains conformation and estimate their conformational entropy." <i>J. Mol. Biol.</i> , 239(2), 249-75.
	Koehl et al. "Mean-field minimization methods for biological macromolecules." <i>Curr Opin Struct Biol.</i> , (1996), 6(2), 222-6.

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msy	Kono et al. "Energy minimization method using automata network for sequence and side-chain conformation prediction from given backbone geometry." <i>Proteins</i> . (1994), 19(3), 244-255.
msy	Kono et al. "Designing the hydrophobic core of <i>Thermus flavus</i> malate dehydrogenase based on side-chain packing." <i>Protein Eng.</i> (1998), 11(1), 47-52.
msy	Kuhlman et al. "Native protein sequences are close to optimal for their structures." <i>Proc. Natl. Acad. Sci. USA</i> . (2000), 97(19), 10383-8.

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msm	Lazar et al. "De novo design of the hydrophobic core of ubiquitin." <i>Protein Sci.</i> (1997), 6(6), 1167-78.
msm	Lazar et al. "Rotamer strain as a determinant of protein structural specificity." <i>Protein Sci.</i> (1999), 8(12), 2598-610.
msm	Lee. "Predicting protein mutant energetics by self-consistent ensemble optimization." <i>J. Mol. Biol.</i> (1994), 236(3), 918-39.

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MSM	Micheletti et al. "Design of proteins with hydrophobic and polar amino acids." <i>Proteins</i> . (1998), 32(1), 80-7.
MSM	Raha et al. "Prediction of amino acid sequence from structure." <i>Protein Sci.</i> (2000), 9(6), 1106-19.
MSM	Ranganathan et al. "Structural and functional analysis of the mitotic rotamase Pin1 suggests substrate recognition is phosphorylation dependent." <i>Cell</i> . (1997), 89(6), 875-86.

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MSM	Street et al. "Computational protein design." <i>Structure Fold Des.</i> (1999), 7(5), R105-9.
MSM	Su et al. "Coupling backbone flexibility and amino acid sequence selection in protein design." <i>Protein Sci.</i> (1997), 6(8), 1701-7.
MSM	Voigt et al. "Trading accuracy for speed: A quantitative comparison of search algorithms in protein sequence design." <i>J. Mol. Biol.</i> (2000), 299(3), 789-803.

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msm	Voigt et al. "Computational method to reduce the search space for directed protein evolution." <i>Proc. Natl. Acad. Sci. USA.</i> (2001), 98(7), 3778-83.
msm	Weiner et al. "A new force field for molecular mechanical simulation of nucleic acids and proteins." <i>Journal of the American Chemical Society.</i> (1984), 106(3), 765-84.

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